

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Barry, Gerard F.
Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.

(ii) TITLE OF INVENTION: Glyphosate Tolerant
5-Enolpyruvylshikimate-3-Phosphate Synthases

(iii) NUMBER OF SEQUENCES: 69

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
(B) STREET: 7000 Chesterfield Village Parkway
(C) CITY: St. Louis
(D) STATE: Missouri
(E) COUNTRY: USA
(F) ZIP: 63198

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/749,611
(B) FILING DATE: 28-AUG-1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/576,537
(B) FILING DATE: 31-AUG-1990
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hoerner Jr., Dennis R.
(B) REGISTRATION NUMBER: 30,914
(C) REFERENCE/DOCKET NUMBER: 38-21(10660)A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (314)537-6099
(B) TELEFAX: (314)537-6047

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATCAAAAT ATTTAGCAGC ATTCCAGATT CGGTTCAATC AACAAAGGTAC GAGCCATATC	60
ACTTTATTCA AATTGGTATC GCCAAAACCA AGAAGGAACT CCCATCCTCA AAGGTTTGTA	120
AGGAAGAATT CTCAGTCCAA AGCCTCAACA AGGTCAAGGGT ACAGAGTCTC CAAACCATTA	180
GCCAAAAGCT ACAGGAGATC AATGAAGAAT CTTCAATCAA AGTAAACTAC TGTTCCAGCA	240
CATGCATCAT GGTCAGTAAG TTTCAGAAAA AGACATCCAC CGAAGACTTA AAGTTAGTGG	300
GCATCTTGAG AAGTAATCTT GTCAACATCG AGCAGCTGGC TTGTGGGGAC CAGACAAAAAA	360
AGGAATGGTG CAGAATTGTT AGGCGCACCT ACCAAAAGCA TCTTTGCCTT TATTGCAAAG	420
ATAAAGCAGA TTCCCTCTAGT ACAAGTGGGG AACAAAATAA CGTGGAAAAG AGCTGTCTG	480
ACAGCCCCACT CACTAATGCG TATGACGAAC GCAGTGACGA CCACAAAAGA ATTCCCTCTA	540
TATAAGAAGG CATTCAATTCC CATTGAGG ATCATCAGAT ACTAACCAAT ATTTCTC	597

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 62..1426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA GGAAGACGCC	60
C ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser	106
1 5 10 15	
TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser	154
20 25 30	
CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile	202
35 40 45	
ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met	250
50 55 60	
CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile	298
65 70 75	
GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp	346
80 85 90 95	
TTC GGC AAT GCC GCC ACG GGC TGC CGC CTG ACC ATG GGC CTC GTC GGG Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly	394
100 105 110	
GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys	442
115 120 125	
CCG CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln	490
130 135 140	

GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGG CCG
Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro 538
145 150 155

AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG
Lys Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln 586
160 165 170 175

GTG AAG TCC GCC GTG CTG CTC GCC GGC CTC AAC ACG CCC GGC ATC ACG
Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr 634
180 185 190

ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG
Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu 682
195 200 205

CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG
Gln Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val 730
210 215 220

CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC
Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile 778
225 230 235

GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC
Asp Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala 826
240 245 250 255

CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC AAC GTG CTG ATG AAC
Leu Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn 874
260 265 270

CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC
Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp 922
275 280 285

ATC GAA GTC ATC AAC CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC
Ile Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp 970
290 295 300

CTG CGC GTT CGC TCC TCC ACG CTG AAG GGC GTC ACG GTG CCG GAA GAC
Leu Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp 1018
305 310 315

CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC
Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala 1066
320 325 330 335

GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC
Ala Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg 1114
340 345 350

GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC
Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu 1162
355 360 365

AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC
Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly 1210
370 375 380

CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GGC GTC GCC
Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala 1258
385 390 395

ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC
Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu 1306
400 405 410 415

GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG
Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr 1354
420 425 430

AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile 1402
435 440 445

GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATGCC ATCGATGGTC
Glu Leu Ser Asp Thr Lys Ala Ala 1456
450 455

CCGCTGCCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTCATC 1516

ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT 1576

CGCTTGATGA CGAGGCCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG 1636

ACCGGTCCGGT CCTGTCGGCC CATGCCATCG GCGAGGCCGGC TTCAAGATC GCGGTCAATGC 1696

CCTCGGTGCG CGGGCGCTG GTCGAGGCCGC AGCGCAGCTT TCGGGCGCGT GAGCCGGCA 1756

CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCC GGATGCGCCG GTGAAGCTCT 1816

ATGTCACCGC GTCACCGGAA GTGGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAATG 1876

CGGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936

TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACTT

1982

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
1 5 10 15

Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
100 105 110

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145 150 155 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
180 185 190
Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205
Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
210 215 220
Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
225 230 235 240
Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255
Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
260 265 270
Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285
Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300
Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
305 310 315 320
Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
325 330 335
Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
340 345 350
Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
355 360 365
Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
370 375 380
Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
385 390 395 400
His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415
Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445
Leu Ser Asp Thr Lys Ala Ala
450 455

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 86..1432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTAGGCCACAC ATAATTACTA TAGCTAGGAA GCCCCGCTATC TCTCAATCCC GCGTGATCGC 60
GCCAAAATGT GACTGTGAAA AATCC ATG TCC CAT TCT GCA TCC CCG AAA CCA 112
Met Ser His Ser Ala Ser Pro Lys Pro 1 5
GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC ATT CCG 160
Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro 10 15 20 25
GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT CTC GCA 208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala 30 35 40
TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC 256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile 45 50 55
AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT AAA GAG
304 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu 50 65 70
GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG TTG CAG 352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln

75	80	85	
CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CGC CTC			
Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu			400
90	95	100	105
ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC			
Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly			448
110	115	120	
GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC CCG TTG			
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu			496
125	130	135	
CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG			
Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro			544
140	145	150	
CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT CGC GTG			
Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val			592
155	160	165	
CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC GGT CTC			
Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly Leu			640
170	175	180	185
AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC			
Asn Thr Pro Gly Val Thr Val Ile Glu Pro Val Met Thr Arg Asp			688
190	195	200	
CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG			
His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu			736
205	210	215	
ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG			
Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys			784
220	225	230	
CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC			
Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala			832
235	240	245	
TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC			
Phe Pro Leu Val Ala Ala Leu Val Glu Gly Ser Asp Val Thr Ile			880
250	255	260	265
CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG			
Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu			928

	270	275	280		
CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly	285	290	295	976	
GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly	300	305	310	1024	
GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA TAT CCG Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro	315	320	325	1072	
GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA GGC GAA ACC GTG ATG GAC Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val Met Asp	330	335	340	1120	
GGG CTC GAC GAA CTG CGC GTC AAG GAA TCG GAT CGT CTG GCA GCG GTC Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Val	350	355	360	1168	
GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC GAG ATG Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly Glu Met	365	370	375	1216	
TCG CTG ACG GTT CGC GGC CGC CCC GAC GGC AAG GGA CTG GGC GGC GGC Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Glu Leu Gly Gly	380	385	390	1264	
ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC CTC GTG Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val	395	400	405	1312	
ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT AAC ATG Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser Asn Met	410	415	420	425	1360
ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly	430	435	440	1408	
GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG "ACAGCGAAAA TATTATTTGC Ala Lys Ile Glu Leu Ser Ile Leu	445			1462	
GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT CTTCCATACG				1522	

TAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC	1582
CTAAGCTTTC TCAAGACTTC GTTAAAATG TACTGAAATC CCGGGGGGTC CGGGGATCAA	1642
ATGACTTCAT TTCTGAGAAA TTGGCCTCGC A	1673

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu			
1	5	10	15
Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His			
20	25	30	
Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr			
35	40	45	
Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln			
50	55	60	
Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn			
65	70	75	80
Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe			
85	90	95	
Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr			
100	105	110	
Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg			
115	120	125	
Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val			
130	135	140	

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
145 150 155 160

Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
355 360 365

Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Gly Thr Val Ala Thr His Leu Asp
385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
405 410 415

Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
420 425 430

Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
435 440 445

Leu :

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGATCGCGC CAAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG 54
Met Ser His Ser Ala Ser Pro
1 5

AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC 102
Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
10 15 20

ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT 150
Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
25 30 35

CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC 198
Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp
40 45 50 55

GTC ATC AAT ACA GCA CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg 60 65 70	246
AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu 75 80 85	294
TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala 90 95 100	342
CGC CTC ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe 105 110 115	390
ATC GGC GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn 120 125 130 135	438
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg 140 145 150	486
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr 155 160 165	534
CGC GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala 170 175 180	582
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr 185 190 195	630
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr 200 205 210 215	678
GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln 220 225 230	726
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser 235 240 245	774

ACC GCC TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val 250 255 260	822
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu 265 270 275	870
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu 280 285 290 295	918
GCA GGC GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu 300 305 310	966
AAG GGC GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu 315 320 325	1014
TAT CCG GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA GGC GAA ACC GTG Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val 330 335 340	1062
ATG GAC GGG CTC GAC GAA CTG CGC GTC AAG GAA TCG GAT CGT CTG GCA Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala 345 350 355	1110
GCG GTC GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly 360 365 370 375	1158
GAG ATG TCG CTG ACG GTT CGC GGC CGC CCC GAC GGC AAG GGA CTG GGC Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly 380 385 390	1206
GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe 395 400 405	1254
CTC GTG ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser 410 415 420	1302
AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly 425 430 435	1350

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAAA
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu 1400
440 445

TATTATTTGC GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT 1460
CTTCCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT 1500
:

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
1 5 10 15

Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
50 55 60

Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
65 70 75 80

Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
85 90 95

Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
100 105 110

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
145 150 155 160
Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175
Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190
Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205
Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220
His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
225 230 235 240
Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255
Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270
Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285
Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300
Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
305 310 315 320
Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
325 330 335
Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
340 345 350
Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
355 360 365
Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
370 375 380
Pro Asp Gly Lys Gly Leu Gly Gly Thr Val Ala Thr His Leu Asp
385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
405 410 415

Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
420 425 430

Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
435 440 445

Leu

:

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Ile Asn Leu
1 5 10 15

Pro Gly Ser Lys Thr Val Ser Asn Arg Ala Leu Leu Leu Ala Ala Leu
20 25 30

Ala His Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp Asp Val
35 40 45

Arg His Met Leu Asn Ala Leu Thr Ala Leu Gly Val Ser Tyr Thr Leu
50 55 60

Ser Ala Asp Arg Thr Arg Cys Glu Ile Ile Gly Asn Gly Gly Pro Leu
65 70 75 80

His Ala Glu Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly Thr Ala
85 90 95

Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Ser Asn Asp Ile Val
100 105 110

Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His Leu Val
115 120 125

Asp Ala Leu Arg Leu Gly Gly Ala Lys Ile Thr Tyr Leu Glu Gln Glu
130 135 140

Asn Tyr Pro Pro Leu Arg Leu Gln Gly Gly Phe Thr Gly Gly Asn Val
145 150 155 160

Asp Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met
165 170 175

Thr Ala Pro Leu Ala Pro Glu Asp Thr Val Ile Arg Ile Lys Gly Asp
180 185 190

Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met Lys Thr
195 200 205

Phe Gly Val Glu Ile Glu Asn Gln His Tyr Gln Gln Phe Val Val Lys
210 215 220

Gly Gly Gln Ser Tyr Gln Ser Pro Gly Thr Tyr Leu Val Glu Gly Asp
225 230 235 240

Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys Gly Gly
245 250 255

Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Met Gln Gly Asp Ile
260 265 270

Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Cys Trp Gly
275 280 285

Asp Asp Tyr Ile Ser Cys Thr Arg Gly Glu Leu Asn Ala Ile Asp Met
290 295 300

Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Ala Ala
305 310 315 320

Leu Phe Ala Lys Gly Thr Thr Arg Leu Arg Asn Ile Tyr Asn Trp Arg
325 330 335

Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu Arg Lys
340 345 350

Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile Thr Pro
355 360 365

Pro Glu Lys Leu Asn Phe Ala Glu Ile Ala Thr Tyr Asn Asp His Arg
370 375 380
Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro Val Thr
385 390 395 400
Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr Phe Glu
: 405 410 415
Gln Leu Ala Arg Ile Ser Gln
420

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATGGCTCA CGGTGCAAGC AGCCGTCCAG CAACTGCTCG TAAGTCCTCT GGTCTTTCTG	60
GAACCGTCCG TATTCCAGGT GACAAGTCTA TCTCCCACAG GTCCTTCATG TTTGGAGGTC	120
TCGCTAGCGG TGAAACTCGT ATCACCGGTC TTTTGGAAAGG TGAAGATGTT ATCAACACTG	180
GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTG.	240
ATGGTGTGAA TAACGGTGGG CTCCTTGCTC CTGAGGCTCC TCTCGATTTC GGTAACGCTG	300
CAACTGGTTG CCGTTTGACT ATGGGTCTTG TTGGTGTGTTA CGATTTCGAT AGCACTTTCA	360
TTGGTGACGC TTCTCTCACT AAGCGTCCAA TGGGTCGTGT GTTGAACCCA CTTCGCGAAA	420
TGGGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGGACCAA	480
AGACTCCAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG	540
TTCTGCTTGC TGGTCTCAAC ACCCCAGGTA TCACCACTGT TATCGAGCCA ATCATGACTC	600
GTGACCACAC TGAAAAAGATG CTTCAAGGTT TTGGTGCTAA CCTTACCGTT GAGACTGATG	660

CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA GCTCACCGGT CAAGTGATTG	720
ATGTTCCAGG TGATCCATCC TCTACTGCTT TCCCATTGGT TGCTGCCTTG CTTGTTCCAG	780
GTTCCGACGT CACCATCCTT AACGTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA	840
CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGGAGAAG	900
ACGTGGCTGA CTTGCGTGT CGTTCTTCTA CTTTGAAGGG TGTTACTGTT CCAGAAGACC	960
GTGCTCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTGCGCTGAAG	1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTTAA GGAAAGCGAC CGTCTTCTG	1080
CTGTCGCAAA CGGTCTCAAG CTCAACGGTG TTGATTGCGA TGAAGGTGAG ACTTCTCTCG	1140
TCGTGCGTGG TCGTCCTGAC GGTAAGGGTC TCGGTAACGC TTCTGGAGCA GCTGTCGCTA	1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC	1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTACTAGCTT CCCAGAGTTC ATGGATTGAA	1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC	1377

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGATCTATCG ATAAGCTTGA TGTAATTGGA GGAAGATCAA AATTTCAAT CCCCATTCTT	60
CGATTGCTTC AATTGAAGTT TCTCCG ATG GCG CAA GTT AGC AGA ATC TGC AAT	113
Met Ala Gln Val Ser Arg Ile Cys Asn	

GGT GTG CAG AAC CCA TCT CTT ATC TCC AAT CTC TCG AAA TCC AGT CAA Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln 10 15 20 25	161
CGC AAA TCT CCC TTA TCG GTT TCT CTG AAG ACG CAG CAG CAT CCA CGA Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg 30 35 40	209
GCT TAT CCG ATT TCG TCG TGG GGA TTG AAG AAG AGT GGG ATG ACG Ala Tyr Pro Ile Ser Ser Trp Gly Leu Lys Ser Gly Met Thr 45 50 55	257
TTA ATT GGC TCT GAG CTT CGT CCT CTT AAG GTC ATG TCT TCT GTT TCC Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser 60 65 70	305
ACG GCG TGC ATG C Thr Ala Cys Met 75	318

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu 1 5 10 15
Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val 20 25 30
Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser 35 40 45
Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg 50 55 60
Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Cys Met 65 70 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 87..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGATCTATCG ATAAGCTTGA TGTAAATTGGA GGAAGATCAA AATTTTCAAT CCCCATTCTT	60
CGATTGCTTC AATTGAAGTT TCTCCG ATG GCG CAA GTT AGC AGA ATC TGC AAT	113
Met Ala Gln Val Ser Arg Ile Cys Asn	
1 5	
GGT GTG CAG AAC CCA TCT CTT ATC TCC AAT CTC TCG AAA TCC AGT CAA	161
Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln	
10 15 20 25	
CGC AAA TCT CCC TTA TCG GTT TCT CTG AAG ACG CAG CAG CAT CCA CGA	209
Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg	
30 35 40	
GCT TAT CCG ATT TCG TCG TGG GGA TTG AAG AAG AGT GGG ATG ACG	257
Ala Tyr Pro Ile Ser Ser Trp Gly Leu Lys Ser Gly Met Thr	
45 50 55	
TTA ATT GGC TCT GAG CTT CGT CCT CTT AAG GTC ATG TCT TCT GTT TCC	305
Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser	
60 65 70	
ACG GCG GAG AAA GCG TCG GAG ATT GTA CTT CAA CCC ATT AGA GAA ATC	353
Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile	
75 80 85	
TCC GGT CTT ATT AAG TTG CCT GGC TCC AAG TCT CTA TCA AAT AGA ATT	401
Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile	
90 95 100 105	
C	402

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
20 25 30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
65 70 75 80

Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
85 90 95

Gly Ser Lys Ser Leu Ser Asn Arg Ile
100 105

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- A) NAME/KEY: CDS
- B) LOCATION: 14..232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGATCTTCAGA ATG GCA CAA ATT AAC AAC ATG GCT CAA GGG ATA CAA	49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln	
1 5 10	
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT	97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser	
15 20 25	
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT	145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn	
30 35 40	
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT	193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys	
45 50 55 60	
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C	233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met	
65 70	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro	
1 5 10 15	
Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu	
20 25 30	
Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val	
35 40 45	
Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile	
50 55 60	

Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

(2) INFORMATION FOR SEO ID NO: 16.

(i) SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 49 351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

AGATCTGCTA GAAATAATT TGTTAACCT TAAGAAGGAG ATATATCC ATG GCA CAA Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn 5 10 15	Met Ala Gln 1	57
TTC CAT AAA CCC CAA GTT CCT AAA TCT TCA AGT TTT CTT GTT TTT GGA Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu Val Phe Gly 20 25 30 35		105
TCT AAA AAA CTG AAA AAT TCA GCA AAT TCT ATG TTG GTT TTG AAA AAA Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys 40 45 50		153
GAT TCA ATT TTT ATG CAA AAG TTT TGT TCC TTT AGG ATT TCA GCA TCA Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser 55 60 65		201
GTG GCT ACA GCA CAG AAG CCT TCT GAG ATA GTG TTG CAA CCC ATT AAA Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys 70 75 80		249
GAG ATT TCA GGC ACT GTT AAA TTG CCT GGC TCT AAA TCA TTA TCT AAT Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn 85 90 95		297
		345

AGA ATT C

Arg Ile

100

352

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
65 70 75 80

Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
85 90 95

Leu Ser Asn Arg Ile
100

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser Gly
1 5 10 15
Leu Xaa Gly Thr Val Arg Ile Pro Gly Asp Lys Met
20 25

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGATHGAYG ARTAYCC

17

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GARGAYGTNA THAACAC

17

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GARGAYGTNA THAATAC

17

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGTGGATAGA TCTAGGAAGA CAACCATGGC TCACGGTC

38

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATAGATTA AGGAAGACGC GCATGCTTCA CGGTGCAAGC AGCC

44

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTGCCCTGA TGAGCTCCAC AATCGCCATC GATGG

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGTCGCTCGT CGTGCCTGGC CGCCCTGACG GC

32

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGCAAGGC CATGCAGGCT ATGGGCGCC

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGGGCTGCCG CCTGACTATG GGCCTCGTCG G

31

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Xaa His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGTBGCSC GYTTSGG

17

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGCAATGCC GCCACCGGCG CGCGCC

26

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGACGGCTGC TTGCACCGTG AAGCATGCTT AAGCTTGGCG TAATCATGG

49

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGAAGACGCC CAGAATTCAC GGTGCAAGCA GCCGG

35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa at position 2 is Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Xaa His Xaa Glu
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Asp Lys Xaa
1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ala Gln Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa at position 2 is Ala Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asn Xaa Thr Arg
1

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro 1 5 10 15	48
GGT GAT AAA TCC ATT TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala 20 25 30	96
GCA GGC ACA ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG Ala Gly Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu 35 40 45	144
AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser 50 55 60	192
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu 65 70 75 80	240
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu 85 90 95	288
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly 100 105 110	336
GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu 115 120 125	384
AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGC GGA GAG TTT ACA Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr 130 135 140	432
CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser 145 150 155 160	480
CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu 165 170 175	528

CAG GCT GAG GGC ACA ACA ACT GTA ACA GAG CCC CAT AAA TCT CGG GAC Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp 180 185 190	576
CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp 195 200 205	624
CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp 210 215 220	672
ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala 225 230 235 240	720
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu 245 250 255	768
AAT CCG ACT CCG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala 260 265 270	816
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly 275 280 285	864
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly 290 295 300	912
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu 305 310 315 320	960
GCG ACT CAG GCG GAA GGA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu 325 330 335	1008
AAA GTG AAA GAA ACA AAC CGT ATT GAT ACT GTT GTT TCT GAG CTT CGC Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg 340 345 350	1056
AAG CTG GGT GCT GAA ATT GAA CCG ACA GCA GAT GGA ATG AAG GTT TAT Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr 355 360 365	1104

GGC AAA CAA ACG TTG AAA GGC GGC GCT GCA GTG TCC AGC CAC GGA GAT	1152		
Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp			
370	375	380	
CAT CGA ATC GGA ATG ATG CTT GGT ATT GCT TCC TGT ATA ACG GAG GAG	1200		
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu			
385	390	395	400
CCG ATT GAA ATC GAG CAC ACG GAT GCC ATT CAC GTT TCT TAT CCA ACC	1248		
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr			
405	410	415	
TTC TTC GAG CAT TTA AAT AAG CTT TCG AAA AAA TCC TGA			
Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	1287		
420	425		

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
1 5 10 15

Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
20 25 30

Ala Gly Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
35 40 45

Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
50 55 60

Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
65 70 75 80

Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
85 90 95

Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly

100 105 110
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
115 120 125
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr
130 135 140
Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
145 150 155 160
Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu
165 170 175
Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp
180 185 190
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp
195 200 205
Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp
210 215 220
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala
225 230 235 240
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu
245 250 255
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala
260 265 270
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly
275 280 285
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly
290 295 300
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu
305 310 315 320
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu
325 330 335
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg
340 345 350

Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr
355 360 365

Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp
370 375 380

His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu
385 390 395 400

Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr
405 410 415

Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser
420 425

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA	48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	
1 5 10 15	
ATA GAA GTG CCG GGC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG	96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	
20 25 30	
GCG TCG CTA GCT GAA GGT GTC TCT ACT ATA TAT AAG CCA CTA CTT GGC	144
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	
35 40 45	

GAA GAT TGT CGT CGT ACG ATG GAC ATT TTC CGA CAC TTA GGT GTA GAA Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu 50 55 60	192
ATC AAA GAA GAT GAT GAA AAA TTA GTT GTG ACT TCC CCA GGA TAT CAA Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln 65 70 75 80	240
GTT AAC ACG CCA CAT CAA GTA TTG TAT ACA GGT AAT TCT GGT ACG ACA Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr 85 90 95	288
ACA CGA TTA TTG GCA GGT TTG TTA AGT GGT TTA GGT AAT GAA AGT GTT Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val 100 105 110	336
TTG TCT GGC GAT GTT TCA ATT GGT AAA AGG CCA ATG GAT CGT GTC TTG Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu 115 120 125	384
AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn 130 135 140	432
TAT ACA CCA TTA ATT ATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr 145 150 155 160	480
CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala 165 170 175	528
AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser 180 185 190	576
CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu 195 200 205	624
GCA GAA GGG TTA TCA ATT AAT ACA ACC CCT GAA GCA ATT CGA TAC ATT Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile 210 215 220	672
AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe 225 230 235 240	720

TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His 245 250 255	768
AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu 260 265 270	816
AAA ATG GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu 275 280 285	864
CCT ACT GCT TCT ATT CGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile 290 295 300	912
ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val 305 310 315 320	960
ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp 325 330 335	1008
GCC GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350	1056
GAT ATG TTA AAC TTG TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365	1104
TTG ATT ATT CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380	1152
ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395 400	1200
AGC GAG CCT GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe 405 410 415	1248
CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly 420 425 430	1293

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
1 5 10 15

Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
20 25 30

Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
35 40 45

Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
50 55 60

Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
65 70 75 80

Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
85 90 95

Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
100 105 110

Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
115 120 125

Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn
130 135 140

Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr
145 150 155 160

Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala
165 170 175

Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser
180 185 190

Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu
195 200 205

Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile
210 215 220

Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe
225 230 235 240

Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His
245 250 255

Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu
260 265 270

Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu
275 280 285

Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile
290 295 300

Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val
305 310 315 320

Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp
325 330 335

Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala
340 345 350

Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
355 360 365

Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
370 375 380

Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
385 390 395 400

Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
405 410 415

Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
420 425 430

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAACATATG AAACGAGATA AGGTGCAG

28

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGAATTCAAA CTTCAGGATC TTGAGATAGA AAATG

35

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGGCCATGG TAAATGAACA AATCATTG

28

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

:

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGGGGAGCTC ATTATCCCTC ATTTTGTAAGC

33

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Leu Thr Asp Glu Thr Leu Val Tyr Pro Phe Lys Asp Ile Pro Ala Asp
1 5 10 15

Gln Gln Lys Val Val Ile Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg
20 25 30

Ala Leu Ile Leu Ala Ala Leu Gly Glu Gly Gln Cys Lys Ile Lys Asn
35 40 45

Leu Leu His Ser Asp Asp Thr Lys His Met Leu Thr Ala Val His Glu
50 55 60

Leu Lys Gly Ala Thr Ile Ser Trp Glu Asp Asn Gly Glu Thr Val Val
65 70 75 80

Val Glu Gly His Gly Gly Ser Thr Leu Ser Ala Cys Ala Asp Pro Leu
85 90 95

Tyr Leu Gly Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Ser Leu Ala
100 105 110

Ala Leu Val Asn Ser Thr Ser Ser Gln Lys Tyr Ile Val Leu Thr Gly
115 120 125

Asn Ala Arg Met Gln Gln Arg Pro Ile Ala Pro Leu Val Asp Ser Leu
130 135 140

Arg Ala Asn Gly Thr Lys Ile Glu Tyr Leu Asn Asn Glu Gly Ser Leu
145 150 155 160

Pro Ile Lys Val Tyr Thr Asp Ser Val Phe Lys Gly Gly Arg Ile Glu
165 170 175

Leu Ala Ala Thr Val Ser Ser Gln Tyr Val Ser Ser Ile Leu Met Cys
180 185 190

Ala Pro Tyr Ala Glu Glu Pro Val Thr Leu Ala Leu Val Gly Gly Lys
195 200 205

Pro Ile Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys
210 215 220

Phe Gly Ile Asn Val Glu Thr Ser Thr Glu Pro Tyr Thr Tyr Tyr
225 230 235 240

Ile Pro Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser
245 250 255

Asp Ala Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly
260 265 270

Thr Thr Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp
275 280 285

Ala Arg Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr
290 295 300

Gln Thr Ala Thr Ser Thr Val Ser Gly Pro Pro Val Gly Thr Leu
305 310 315 320

Lys Pro Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu
325 330 335

Thr Ala Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser
340 345 350

Ala Asn Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu
355 360 365

Cys Asn Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val
370 375 380

Lys Thr Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser
385 390 395 400

Ile Lys Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val
: 405 410 415

Cys Thr Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala
420 425 430

Gly Met Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val
435 440 445

Arg Ile Leu Glu Arg His Cys Thr Gly Lys Thr Trp Pro Gly Trp Trp
450 455 460

Asp Val Leu His Ser Glu Leu Gly Ala Lys Leu Asp Gly Ala Glu Pro
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Ala Pro Ser Ile Glu Val His Pro Gly Val Ala His Ser Ser Asn
1 5 10 15

Val Ile Cys Ala Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg Ala Leu
20 25 30

Val Leu Ala Ala Leu Gly Ser Gly Thr Cys Arg Ile Lys Asn Leu Leu
35 40 45

His Ser Asp Asp Thr Glu Val Met Leu Asn Ala Leu Glu Arg Leu Gly
50 55 60

Ala Ala Thr Phe Ser Trp Glu Glu Glu Gly Glu Val Leu Val Val Asn
65 70 75 80

Gly Lys Gly Gly Asn Leu Gln Ala Ser Ser Ser Pro Leu Tyr Leu Gly
85 90 95

Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Thr Val Ala Thr Leu Ala
100 105 110

Asn Ser Ser Thr Val Asp Ser Ser Val Leu Thr Gly Asn Asn Arg Met
115 120 125

Lys Gln Arg Pro Ile Gly Asp Leu Val Asp Ala Leu Thr Ala Asn Val
130 135 140

Leu Pro Leu Asn Thr Ser Lys Gly Arg Ala Ser Leu Pro Leu Lys Ile
145 150 155 160

Ala Ala Ser Gly Gly Phe Ala Gly Gly Asn Ile Asn Leu Ala Ala Lys
165 170 175

Val Ser Ser Gln Tyr Val Ser Ser Leu Leu Met Cys Ala Pro Tyr Ala
180 185 190

Lys Glu Pro Val Thr Leu Arg Leu Val Gly Gly Lys Pro Ile Ser Gln
195 200 205

Pro Tyr Ile Asp Met Thr Thr Ala Met Met Arg Ser Phe Gly Ile Asp
210 215 220

Val Gln Lys Ser Thr Thr Glu Glu His Thr Tyr His Ile Pro Gln Gly
225 230 235 240

Arg Tyr Val Asn Pro Ala Glu Tyr Val Ile Glu Ser Asp Ala Ser Cys
245 250 255

Ala Thr Tyr Pro Leu Ala Val Ala Val Thr Gly Thr Thr Cys Thr
260 265 270

Val Pro Asn Ile Gly Ser Ala Ser Leu Gln Gly Asp Ala Arg Phe Ala
275 280 285

Val Glu Val Leu Arg Pro Met Gly Cys Thr Val Glu Gln Thr Glu Thr
290 295 300

Ser Thr Thr Val Thr Gly Pro Ser Asp Gly Ile Leu Arg Ala Thr Ser
305 310 315 320
Lys Arg Gly Tyr Gly Thr Asn Asp Arg Cys Val Pro Arg Cys Phe Arg
325 330 335
Thr Gly Ser His Arg Pro Met Glu Lys Ser Gln Thr Thr Pro Pro Val
340 345 350
Ser Ser Gly Ile Ala Asn Gln Arg Val Lys Glu Cys Asn Arg Ile Lys
355 360 365
Ala Met Lys Asp Glu Leu Ala Lys Phe Gly Val Ile Cys Arg Glu His
370 375 380
Asp Asp Gly Leu Glu Ile Asp Gly Ile Asp Arg Ser Asn Leu Arg Gln
385 390 395 400
Pro Val Gly Val Phe Cys Tyr Asp Asp His Arg Val Ala Phe Ser
405 410 415
Phe Ser Val Leu Ser Leu Val Thr Pro Gln Pro Thr Leu Ile Leu Glu
420 425 430
Lys Glu Cys Val Gly Lys Thr Trp Pro Gly Trp Trp Asp Thr Leu Arg
435 440 445
Gln Leu Phe Lys Val Lys Leu Glu Gly Lys Glu Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15

Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45

Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Lys Leu Gly Leu Asn
50 55 60

Val Glu Arg Asp Ser Val Asn Asn Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80

Gly Ile Phe Pro Ala Ser Leu Asp Ser Lys Ser Asp Ile Glu Leu Tyr
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
145 150 155 160

Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Thr Gly Pro Ser Arg Asp Ala Phe Gly Met Arg His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
370 375 380

Val Ile Thr Pro Pro Ala Lys Val Lys Pro Ala Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Gln Val Leu Glu Ser Ile Thr Lys His
435 440

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15

Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45

Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn
50 55 60

Val Glu Thr Asp Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80

Gly Ile Phe Pro Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
145 150 155 160

Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Cys Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Asp Ala Phe Gly Met Arg His Leu Arg
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
370 375 380

Val Ile Thr Pro Pro Lys Lys Val Lys Thr Ala Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Ile Thr Ile Asn Asp Ser Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Gln Val Leu Glu Arg Ile Thr Lys His
435 440

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Pro Asn Glu Ile Val Leu Gln Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

•

Ala Ala Leu Ser Lys Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
65 70 75 80

Gly Gln Phe Pro Val Gly Lys Ser Glu Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
210 215 220

Glu His Thr Ser Ser Trp Asp Lys Phe Leu Val Arg Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
435 440

(2) INFORMATION FOR SEQ ID NO:54:

- i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Pro His Glu Ile Val Leu Xaa Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
65 70 75 80

Gly Gln Phe Pro Val Gly Lys Lys Ser Glu Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Ser Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Phe Val
210 215 220

Glu His Ser Ser Gly Trp Asp Arg Phe Leu Val Lys Gly Gly Gln Lys
225 230 235 240
Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
245 250 255
Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
260 265 270
Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285
Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300
Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
305 310 315 320
Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335
Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350
Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365
Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
370 375 380
Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
385 390 395 400
Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415
Val Pro Val Thr Ile Lys Asn Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430
Asp Tyr Phe Glu Val Leu Gln Lys Tyr Ser Lys His
435 440

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Glu Asp Ser Ala Asn Gln Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80

Gly Leu Phe Pro Val Gly Lys Glu Ser Lys Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly Asn Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Ser Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Lys Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Ile Ser Val
210 215 220

Glu His Ser Ser Ser Trp Asp Arg Phe Phe Val Arg Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Ile Thr Val
260 265 270

Glu Gly Cys Gly Thr Asn Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Ser Ser Ser Gly Arg Lys His Leu Arg
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Tyr Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Asp Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
435 440

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
1 5 10 15

Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
20 25 30

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 90

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Pro
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Pro Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Lys Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415
Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Val
1 5 10 15
Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30
Ala Leu Ala Arg Gly Thr Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45
Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Val His Tyr
50 55 60
Val Leu Ser Ser Asp Arg Thr Arg Cys Glu Val Thr Gly Thr Gly Gly
65 70 75 80
Pro Leu Gin Ala Gly Ser Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95
Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Ser Asn Asp
100 105 110
Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125
Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Thr Gly Gly
145 150 155 160
Asp Val Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175
Leu Met Ala Ser Pro Leu Ala Pro Gln Asp Thr Val Ile Ala Ile Lys
180 185 190
Gly Glu Leu Val Ser Arg Pro Tyr Ile Asp Ile Thr Leu His Leu Met
195 200 205
Lys Thr Phe Gly Val Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Ile
210 215 220
Val Arg Gly Asn Gln Gln Tyr Gln Ser Pro Gly Asp Tyr Leu Val Glu
225 230 235 240
Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
245 250 255
Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Val Gln Gly
260 265 270
Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Val Thr
275 280 285
Trp Gly Glu Asp Tyr Ile Ala Cys Thr Arg Gly Glu Leu Asn Ala Ile
290 295 300
Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320
Ala Ala Leu Phe Ala Arg Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335
Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350
Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Tyr Ile Arg Ile
355 360 365
Thr Pro Pro Leu Thr Leu Gln Phe Ala Glu Ile Gly Thr Tyr Asn Asp
370 375 380
His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Gly Gln Leu Ala Arg Ile Ser Thr Leu Ala
420 425

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Leu Glu Ser Leu Thr Leu His Pro Ile Ala Leu Ile Asn Gly Thr
1 5 10 15

Val Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu
20 25 30

Ala Ala Leu Ala Glu Gly Thr Thr Gln Leu Asn Asn Leu Leu Asp Ser
35 40 45

Asp Asp Ile Arg His Met Leu Asn Ala Leu Gln Ala Leu Gly Val Lys
50 55 60

Tyr Arg Leu Ser Ala Asp Arg Thr Arg Cys Glu Val Asp Gly Leu Gly
65 70 75 80

Gly Lys Leu Val Ala Glu Gln Pro Leu Glu Leu Phe Leu Gly Asn Ala
85 90 95

Gly Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Lys Asn
100 105 110

Asp Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly
115 120 125

His Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu
130 135 140

Glu Gln Glu Asn Tyr Arg Arg Cys Ile Ala Gly Gly Phe Arg Gly Gly
145 150 155 160

Lys Leu Thr Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Glu Gln Asp Thr Glu Ile Gln Ile Gln
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Leu Met
195 200 205

Lys Ala Phe Gly Val Asp Val Val His Glu Asn Tyr Gln Ile Phe His
210 215 220

Ile Lys Gly Gly Gln Thr Tyr Arg Ser Pro Gly Ile Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys
245 250 255

Gly Gly Thr Val Arg Val Thr Gly Ile Gly Lys Gln Ser Val Gln Gly
260 265 270

Asp Thr Lys Phe Ala Asp Val Leu Glu Lys Met Gly Ala Lys Ile Ser
275 280 285

Trp Gly Asp Asp Tyr Ile Glu Cys Ser Arg Gly Glu Leu Gln Gly Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Asp Gly Pro Thr Val Ile Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Ser Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly Gln Asp Tyr Ile Arg Val
355 360 365

Val Pro Pro Ala Gln Leu Ile Ala Ala Glu Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415
Phe Glu Gln Leu Ala Arg Leu Ser Gln Ile Ala
420 425

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Glu Lys Ile Thr Leu Ala Pro Ile Ser Ala Val Glu Gly Thr Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Lys Gly Thr Thr Lys Val Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Ile Arg His Met Leu Asn Ala Leu Lys Ala Leu Gly Val Arg Tyr
50 55 60

Gln Leu Ser Asp Asp Lys Thr Ile Cys Glu Ile Glu Gly Leu Gly Gly
65 70 75 80

Ala Phe Asn Ile Gln Asp Asn Leu Ser Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu Lys Gly Asn His
100 105 110

Glu Val Glu Ile Ile Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro
115 120 125

Ile Leu His Leu Val Asp Ala Leu Arg Gln Ala Gly Ala Asp Ile Arg
130 135 140

Tyr Leu Glu Asn Glu Glu Gly Tyr Pro Pro Leu Ala Ile Arg Asn Lys Gly
145 150 155 160

Ile Lys Gly Gly Lys Val Lys Ile Asp Gly Ser Ile Ser Ser Gln Phe
165 170 175

Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala Glu Asn Asp Thr Glu
180 185 190

Ile Glu Ile Ile Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr
195 200 205

Leu Ala Met Met Arg Asp Phe Gly Val Lys Val Glu Asn His His Tyr
210 215 220

Gln Lys Phe Gln Val Lys Gly Asn Gln Ser Tyr Ile Ser Pro Asn Lys
225 230 235 240

Tyr Leu Val Glu Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala
245 250 255

Gly Ala Ile Lys Gly Lys Val Lys Val Thr Gly Ile Gly Lys Asn Ser
260 265 270

Ile Gln Gly Asp Arg Leu Phe Ala Asp Val Leu Glu Lys Met Gly Ala
275 280 285

Lys Ile Thr Trp Gly Glu Asp Phe Ile Gln Ala Glu His Ala Glu Leu
290 295 300

Asn Gly Ile Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr
305 310 315 320

Ile Ala Thr Thr Ala Leu Phe Ser Asn Gly Glu Thr Val Ile Arg Asn
325 330 335

Ile Tyr Asn Trp Arg Val Lys Glu Thr Asp Arg Leu Thr Ala Met Ala
340 345 350

Thr Glu Leu Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Phe
355 360 365

Ile Arg Ile Gln Pro Leu Ala Leu Asn Gln Phe Lys His Ala Asn Ile
370 375 380

Glu Thr Tyr Asn Asp His Arg Met Ala Met Cys Phe Ser Leu Ile Ala
385 390 395 400

Leu Ser Asn Thr Pro Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys
405 410 415

Thr Phe Pro Thr Phe Phe Asn Glu Phe Glu Lys Ile Cys Leu Lys Asn
420 425 430

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Val Ile Lys Asp Ala Thr Ala Ile Thr Leu Asn Pro Ile Ser Tyr Ile
1 5 10 15

Glu Gly Glu Val Arg Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala
20 25 30

Leu Leu Leu Ser Ala Leu Ala Lys Gly Lys Thr Thr Leu Thr Asn Leu
35 40 45

Leu Asp Ser Asp Asp Val Arg His Met Leu Asn Ala Leu Lys Glu Leu
50 55 60

Gly Val Thr Tyr Gln Leu Ser Glu Asp Lys Ser Val Cys Glu Ile Glu
65 70 75 80

Gly Leu Gly Arg Ala Phe Glu Trp Gln Ser Gly Leu Ala Leu Phe Leu
85 90 95

Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu
100 105 110

Ser Thr Pro Asn Arg Glu Gly Lys Asn Glu Ile Val Leu Thr Gly Glu
115 120 125

Pro Arg Met Lys Glu Arg Pro Ile Gln His Leu Val Asp Ala Leu Cys
130 135 140

Gln Ala Gly Ala Glu Ile Gln Tyr Leu Glu Gln Glu Gly Tyr Pro Pro
145 150 155 160

Ile Ala Ile Arg Asn Thr Gly Leu Lys Gly Gly Arg Ile Gln Ile Asp
165 170 175

Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met Ala Ala Pro
180 185 190
•

Met Ala Glu Ala Asp Thr Glu Ile Glu Ile Ile Gly Glu Leu Val Ser
195 200 205

Lys Pro Tyr Ile Asp Ile Thr Leu Lys Met Met Gln Thr Phe Gly Val
210 215 220

Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Leu Val Lys Gly His Gln
225 230 235 240

Gln Tyr Gln Ser Pro His Arg Phe Leu Val Glu Gly Asp Ala Ser Ser
245 250 255

Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys Gly Lys Val Lys Val
260 265 270

Thr Gly Val Gly Lys Asn Ser Ile Gln Gly Asp Arg Leu Phe Ala Asp
275 280 285

Val Leu Glu Lys Met Gly Ala His Ile Thr Trp Gly Asp Asp Phe Ile
290 295 300

Gln Val Glu Lys Gly Asn Leu Lys Gly Ile Asp Met Asp Met Asn His
305 310 315 320

Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Thr Ala Leu Phe Ala Glu
325 330 335

Gly Glu Thr Val Ile Arg Asn Ile Tyr Asn Trp Arg Val Lys Glu Thr
340 345 350

Asp Arg Leu Thr Ala Met Ala Thr Glu Leu Arg Lys Val Gly Ala Glu
355 360 365

Val Glu Glu Gly Glu Asp Phe Ile Arg Ile Gln Pro Leu Asn Leu Ala
370 375 380

Gln Phe Gln His Ala Glu Leu Asn Ile His Asp His Arg Met Ala Met
385 390 395 400

Cys Phe Ala Leu Ile Ala Leu Ser Lys Thr Ser Val Thr Ile Leu Asp
405 410 415
Pro Ser Cys Thr Ala Lys Thr Phe Pro Thr Phe Leu Ile Leu Phe Thr
420 425 430
Leu Asn Thr Arg Glu Val Ala Tyr Arg
435 440

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Asn Ser Leu Arg Leu Glu Pro Ile Ser Arg Val Ala Gly Glu Val Asn
1 5 10 15
Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala Ala
20 25 30
Leu Ala Arg Gly Thr Thr Arg Leu Thr Asn Leu Leu Asp Ser Asp Asp
35 40 45
Ile Arg His Met Leu Ala Ala Leu Thr Gln Leu Gly Val Lys Tyr Lys
50 55 60
Leu Ser Ala Asp Lys Thr Glu Cys Thr Val His Gly Leu Gly Arg Ser
65 70 75 80
Phe Ala Val Ser Ala Pro Val Asn Leu Phe Leu Gly Asn Ala Gly Thr
85 90 95
Ala Met Arg Pro Leu Cys Ala Ala Leu Cys Leu Gly Ser Gly Glu Tyr
100 105 110
Met Leu Gly Gly Glu Pro Arg Met Gln Glu Arg Pro Ile Gly His Leu
115 120 125
Val Asp Cys Leu Ala Leu Lys Gly Ala His Ile Gln Tyr Leu Lys Lys
130 135 140

Asp Gly Tyr Pro Pro Leu Val Val Asp Ala Lys Gly Leu Trp Gly Gly
145 150 155 160
Asp Val His Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Phe
165 170 175
Leu Met Ala Ala Pro Ala Met Ala Pro Val Ile Pro Arg Ile His Ile
180 185 190
Lys Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Ile
195 200 205
Met Asn Ser Ser Gly Val Val Ile Glu His Asp Asn Tyr Lys Leu Phe
210 215 220
Tyr Ile Lys Gly Asn Gln Ser Ile Val Ser Pro Gly Asp Phe Leu Val
225 230 235 240
Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile
245 250 255
Lys Gly Lys Val Arg Val Thr Gly Ile Gly Lys His Ser Ile Gly Asp
260 265 270
Ile His Phe Ala Asp Val Leu Glu Arg Met Gly Ala Arg Ile Thr Trp
275 280 285
Gly Asp Asp Phe Ile Glu Ala Glu Gln Gly Pro Leu His Gly Val Asp
290 295 300
Met Asp Met Asn His Ile Pro Asp Val Gly His Asp His Ser Gly Gln
305 310 315 320
Ser His Cys Leu Pro Arg Val Pro Pro His Ser Gln His Leu Gln Leu
325 330 335
Ala Val Arg Asp Asp Arg Cys Thr Pro Cys Thr His Gly His Arg Arg
340 345 350
Ala Gln Ala Gly Val Ser Glu Glu Gly Thr Thr Phe Ile Thr Arg Asp
355 360 365
Ala Ala Asp Pro Ala Gln Ala Arg Arg Asp Arg His Leu Gln Arg Ser
370 375 380
Arg Ile Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Ile Ala Val
385 390 395 400

Thr Ile Asn Asp Pro Gly Cys Thr Ser Lys Thr Phe Pro Asp Tyr Phe
405 410 415
Asp Lys Leu Ala Ser Val Ser Gln Ala Val
420 425

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ser Gly Leu Ala Tyr Leu Asp Leu Pro Ala Ala Arg Leu Ala Arg
1 5 10 15

Gly Glu Val Ala Leu Pro Gly Ser Lys Ser Ile Ser Asn Arg Val Leu
20 25 30

Leu Leu Ala Ala Leu Ala Glu Gly Ser Thr Glu Ile Thr Gly Leu Leu
35 40 45

Asp Ser Asp Asp Thr Arg Val Met Leu Ala Ala Leu Arg Gln Leu Gly
50 55 60

Val Ser Val Gly Glu Val Ala Asp Gly Cys Val Thr Ile Glu Gly Val
65 70 75 80

Ala Arg Phe Pro Thr Glu Gln Ala Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Phe Arg Pro Leu Thr Ala Ala Leu Ala Leu Met Gly Gly Asp
100 105 110

Tyr Arg Leu Ser Gly Val Pro Arg Met His Glu Arg Pro Ile Gly Asp
115 120 125

Leu Val Asp Ala Leu Arg Gln Phe Gly Ala Gly Ile Glu Tyr Leu Gly
130 135 140

Gln Ala Gly Tyr Pro Pro Leu Arg Ile Gly Gly Gly Ser Ile Arg Val
145 150 155 160
Asp Gly Pro Val Arg Val Glu Gly Ser Val Ser Ser Gln Phe Leu Thr
165 170 175
Ala Leu Leu Met Ala Ala Pro Val Leu Ala Arg Arg Ser Gly Gln Asp
180 185 190
Ile Thr Ile Glu Val Val Gly Glu Leu Ile Ser Lys Pro Tyr Ile Glu
195 200 205
Ile Thr Leu Asn Leu Met Ala Arg Phe Gly Val Ser Val Arg Arg Asp
210 215 220
Gly Trp Arg Ala Phe Thr Ile Ala Arg Asp Ala Val Tyr Arg Gly Pro
225 230 235 240
Gly Arg Met Ala Ile Glu Gly Asp Ala Ser Thr Ala Ser Tyr Phe Leu
245 250 255
Ala Leu Gly Ala Ile Gly Gly Pro Val Arg Val Thr Gly Val Gly
260 265 270
Glu Asp Ser Ile Gln Gly Asp Val Ala Phe Ala Ala Thr Leu Ala Ala
275 280 285
Met Gly Ala Asp Val Arg Tyr Gly Pro Gly Trp Ile Glu Thr Arg Gly
290 295 300
Val Arg Val Ala Glu Gly Gly Arg Leu Lys Ala Phe Asp Ala Asp Phe
305 310 315 320
Asn Leu Ile Pro Asp Ala Ala Met Thr Ala Ala Thr Leu Ala Leu Tyr
325 330 335
Ala Asp Gly Pro Cys Arg Leu Arg Asn Ile Gly Ser Trp Arg Val Lys
340 345 350
Glu Thr Asp Arg Ile His Ala Met His Thr Glu Leu Glu Lys Leu Gly
355 360 365
Ala Gly Val Gln Ser Gly Ala Asp Trp Leu Glu Val Ala Pro Pro Glu
370 375 380
Pro Gly Gly Trp Arg Asp Ala His Ile Gly Thr Trp Asp Asp His Arg
385 390 395 400

Met Ala Met Cys Phe Leu Leu Ala Ala Phe Gly Pro Ala Ala Val Arg
405 410 415
Ile Leu Asp Pro Gly Cys Val Ser Lys Thr Phe Pro Asp Tyr Phe Asp
420 425 430
Val Tyr Ala Gly Leu Leu Ala Ala Arg Asp
435 440

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15
Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30
Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45
Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60
Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80
Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95
Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110
Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400
Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415
Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1894 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 275..1618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGGGCTGTA ACGGTAGTAG GGGTCCCGAG CACAAAAGCG GTGCCGGCAA GCAGAACTAA 60
TTTCCATGGG GAATAATGGT ATTCATTGG TTTGGCCTCT GGTCTGGCAA TGGTTGCTAG 120
GCGATCGCCT GTTGAAATTAA ACAAACTGTC GCCCTTCCAC TGACCATGGT AACGATGTTT 180
TTTACTTCCT TGACTAACCG AGGAAAATTG GGCGGGGGGC AGAAATGCCA ATACAATTAA 240
GCTTGGTCTT CCCTGCCCTT AATTGTCCC CTCC ATG GCC TTG CTT TCC CTC 292
Met Ala Leu Leu Ser Leu
1 5

AAC AAT CAT CAA TCC CAT CAA CGC TTA ACT GTT AAT CCC CCT GCC CAA 340
Asn Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln
10 15 20

GGG GTC GCT TTG ACT GGC CGC CTA AGG GTG CCG GGG GAT AAA TCC ATT 388
Gly Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile
25 30 35

TCC CAT CGG GCC TTG ATG TTG GGG GCG ATC GCC ACC GGG GAA ACC ATT 436
Ser His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile
40 45 50

ATC GAA GGG CTA CTG TTG GGG GAA GAT CCC CGT AGT ACG GCC CAT TGC 484
Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys
55 60 65 70

TTT CGG GCC ATG GGA GCA GAA ATC AGC GAA CTA AAT TCA GAA AAA ATC 532
Phe Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile
75 80 85

ATC GTT CAG GGT CGG GGT CTG GGA CAG TTG CAG GAA CCC AGT ACC GTT 580
Ile Val Gln Gly Arg Gly Leu Gly Gln Leu Gln Glu Pro Ser Thr Val
90 95 100

TTG GAT GCG GGG AAC TCT GGC ACC ACC ATG CGC TTA ATG TTG GGC TTG 628
Leu Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu
105 110 115

CTA GCC GGG CAA AAA GAT TGT TTA TTC ACC GTC ACC GGC GAT GAT TCC 676
Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Asp Ser
120 125 130

CTC CGT CAC CGC CCC ATG TCC CGG GTA ATT CAA CCC TTG CAA CAA ATG 724
Leu Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met
135 140 145 150

GGG GCA AAA ATT TGG GCC CGG AGT AAC GGC AAG TTT GCG CCG CTG GCA 772
Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala
155 160 165

GTC CAG GGT AGC CAA TTA AAA CCG ATC CAT TAC CAT TCC CCC ATT GCT 820
Val Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala
170 175 180

TCA GCC CAG GTA AAG TCC TGC CTG TTG CTA CGG GGG TTA ACC ACC GAG 868
Ser Ala Gln Val Lys Ser Cys Leu Leu Ala Gly Leu Thr Thr Glu
185 190 195

GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CGG GAT CAT AGC GAA 916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu
200 205 210

CGC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC 964
Arg Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr
215 220 225 230

CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG His Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val 235 240 245 1012
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala 250 255 260 265 1060
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn 265 270 275 1108
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp 280 285 290 1156
ATT ACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 295 300 305 310 1204
CTG CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 315 320 325 1252
ATT ATT CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340 1300
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 345 350 355 1348
GTT AAA GAA AGC GAT CGC CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 360 365 370 1396
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 375 380 385 390 1444
GGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg 395 400 405 1492
ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGG GGG CAA ACA Ile Ala Met Ala Leu Ala Ile Ala Leu Gly Ser Gly Gly Gln Thr 410 415 420 1540

ATT ATT AAC CGG GCG GAA GCG GCC GCC ATT TCC TAT CCA GAA TTT TTT Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe 425 430 435	1588
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG Gly Thr Leu Gly Gln Val Ala Gln Gly 440 445	1635
GGCGGTTTGT AAATGTTTA CCAAGGTAGT TTGGGGTAAA GGCCCCAGCA AGTGCTGCCA GGGTAATTAA TCCGCAATTG ACCAATCGGC ATGGACCGTA TCGTTCAAAC TGGGTAATTC TCCCTTTAAT TCCTTAAAG CTCGCTTAAA ACTGCCAAC GTATCTCCGT AATGGCGAGT GAGTAGAAGT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAAGCCT GCATCACTGA CCACTTATAA CTTTCGGGA	1695 1755 1815 1875
	1894

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ala Leu Leu Ser Leu Asn Asn His Gln Ser His Gln Arg Leu Thr
1 5 10 15

Val Asn Pro Pro Ala Gln Gly Val Ala Leu Thr Gly Arg Leu Arg Val
20 25 30

Pro Gly Asp Lys Ser Ile Ser His Arg Ala Leu Met Leu Gly Ala Ile
35 40 45

Ala Thr Gly Glu Thr Ile Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro
50 55 60

Arg Ser Thr Ala His Cys Phe Arg Ala Met Gly Ala Glu Ile Ser Glu
65 70 75 80

Leu Asn Ser Glu Lys Ile Ile Val Gln Gly Arg Gly Leu Gly Gln Leu
85 90 95

Gln Glu Pro Ser Thr Val Leu Asp Ala Gly Asn Ser Gly Thr Thr Met
100 105 110

Arg Leu Met Leu Gly Leu Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr
115 120 125

Val Thr Gly Asp Asp Ser Leu Arg His Arg Pro Met Ser Arg Val Ile
130 135 140

Gln Pro Leu Gln Gln Met Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly
145 150 155 160

Lys Phe Ala Pro Leu Ala Val Gln Gly Ser Gln Leu Lys Pro Ile His
165 170 175

Tyr His Ser Pro Ile Ala Ser Ala Gln Val Lys Ser Cys Leu Leu Leu
180 185 190

Ala Gly Leu Thr Thr Glu Gly Asp Thr Thr Val Thr Glu Pro Ala Leu
195 200 205

Ser Arg Asp His Ser Glu Arg Met Leu Gln Ala Phe Gly Ala Lys Leu
210 215 220

Thr Ile Asp Pro Val Thr His Ser Val Thr Val His Gly Pro Ala His
225 230 235 240

Leu Thr Gly Gln Arg Val Val Val Pro Gly Asp Ile Ser Ser Ala Ala
245 250 255

Phe Trp Leu Val Ala Ala Ser Ile Leu Pro Gly Ser Glu Leu Leu Val
260 265 270

Glu Asn Val Gly Ile Asn Pro Thr Arg Thr Gly Val Leu Glu Val Leu
275 280 285

Ala Gln Met Gly Ala Asp Ile Thr Pro Glu Asn Glu Arg Leu Val Thr
290 295 300

Gly Glu Pro Val Ala Asp Leu Arg Val Arg Ala Ser His Leu Gln Gly
305 310 315 320

Cys Thr Phe Gly Gly Glu Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro
325 330 335

Ile Leu Ala Val Ala Ala Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu
340 345 350

Asp Ala Ala Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Ile
355 360 365

Ala Ser Glu Leu Gly Lys Met Gly Ala Lys Val Thr Glu Phe Asp Asp
370 375 380

Gly Leu Glu Ile Gln Gly Gly Ser Pro Leu Gln Gly Ala Glu Val Asp
385 390 395 400

Ser Leu Thr Asp His Arg Ile Ala Met Ala Leu Ala Ile Ala Ala Leu
405 410 415

Gly Ser Gly Gly Gln Thr Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile
420 425 430

Ser Tyr Pro Glu Phe Phe Gly Thr Leu Gly Gln Val Ala Gln Gly
435 440 445

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTTAAAAACA ATGAGTTAAA AAATTATTTT TCTGGCACAC GCGCTTTTT TGCATTTTTT 60
CTCCCATTTT TCCGGCACAA TAACGTTGGT TTTATAAAAG GAAATG ATG ATG ACG 115
Met Met Thr
1

AAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG 163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
5 10 15

ATA TGC GGC GAT AAA TCA ATG TCG CAT CGC GCC TTA TTA TTA GCA GCG Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala 20 25 30 35	211
TTA GCA GAA GGA CAA ACG GAA ATC CGC GGC TTT TTA GCG TGC GCG GAT Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp 40 45 50	259
TGT TTG GCG ACG CGG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln 55 60 65	307
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu 70 75 80	355
CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met 85 90 95	403
CGT TTA TTG GCA GGA ATT TTG GCA GCG CAG CGC TTT GAG AGC GTG TTA Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu 100 105 110 115	451
TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr 120 125 130	499
CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr 135 140 145	547
GCG CCG TTA CAT ATT TCA GGA CGC CCG CTG ACC GGC ATT GAT TAC GCG Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala 150 155 160	595
TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly 165 170 175	643
TTA TTG GCT GAC GGT ACC ACG CGG CTG CAT ACT TGC GGC ATC AGT CGC Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg 180 185 190 195	691
GAC CAC ACG GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile 200 205 210	739

AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC
Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys 787
215 220 225

GTG CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val 835
230 235 240

GCG GCT TTG ATT GCG CCG CGC GCG GAA GTC GTT ATT CGT AAT GTC GGC
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg Asn Val Gly 883
245 250 255

ATT AAT CCG ACG CGG GCG GCA ATC ATT ACT TTG TTG CAA AAA ATG GGC
Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly 931
260 265 270 275

GGA CGG ATT GAA TTG CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG
Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val 979
280 285 290

GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CGC GGC ATT ACG GTG GCG
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala 1027
295 300 305

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile 1075
310 315 320

GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA
Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu 1123
325 330 335

TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu 1171
340 345 350 355

CAA ACT TTG GGC GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile 1219
360 365 370

TAT GGA AGA AGC GAT CGG CAA TTT TTA CCG GCG CGG GTG AAC AGT TTT
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe 1267
375 380 385

GCG GAT CAT CGG ATT CGG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala 1315
390 395 400

GCA GGT GAA TTA TTG ATT GAT GAC GGC GCG GTG GCG GCG GTT TCT ATG 1363
Ala Gly Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met
405 410 415

CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA 1411
Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu
420 425 430 435

AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTTG GAAAAGGCAC 1465
Lys Asp Ala Lys Asn Cys His Asp
440

GGTGGCGCAA GCTT 1479

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Met Thr Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly
1 5 10 15

Glu Ile Thr Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu
20 25 30

Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala
35 40 45

Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val
50 55 60

Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe
65 70 75 80

Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly
85 90 95

Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu
100 105 110

Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg
115 120 125
Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser
130 135 140
Asn Phe Thr Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile
145 150 155 160
Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile
165 170 175
Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly
180 185 190
Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala
195 200 205
Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu
210 215 220
His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe
225 230 235 240
Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg
245 250 255
Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln
260 265 270
Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala
275 280 285
Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile
290 295 300
Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile
305 310 315 320
Phe Phe Ile Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn
325 330 335
Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala
340 345 350
Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
355 360 365

Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
370 375 380
Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
385 390 395 400
Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
405 410 415
Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
420 425 430
Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
435 440